STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/700, 8/6A_

Source: _1Fw16_

Date Processed by STIC: _7/14/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/700, 816A_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
____Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2____Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
____Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
____"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for **each** skipped sequence:
____(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
____(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
____(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
____Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s) _16_ missing the <220> "Feature" and associated numeric identifiers and responses. Use
of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
____"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/700,816A**

DATE: 07/14/2006
TIME: 09:11:02

Input Set : **A:\new SEQLIST txt.txt**
Output Set: **N:\CRF4\07142006\J700816A.raw**

```
 4 <110> APPLICANT: Xu, Zuoshang and Zamore, Phillip D.
 6 <120> TITLE OF INVENTION: Allele-Specific RNA Interference
 9 <130> FILE REFERENCE: UMY-038
11 <140> CURRENT APPLICATION NUMBER: 10/700816A
12 <141> CURRENT FILING DATE: 2003-11-04
14 <150> PRIOR APPLICATION NUMBER: 60/423,507
15 <151> PRIOR FILING DATE: 2002-11-04
17 <150> PRIOR APPLICATION NUMBER: 60/488,283
18 <151> PRIOR FILING DATE: 2003-07-18
20 <160> NUMBER OF SEQ ID NOS: 19
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

see pp 2-3, 5

Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

p.2

```
280 <210> SEQ ID NO: 19
281 <211> LENGTH: 2288
282 <212> TYPE: DNA
283 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 19
286 gtaccctgtt tacatcattt tgccattttc gcgtactgca accggcgggc cacgccgtga 60
287 aaagaaggtt gttttctcca cagtttcggg gttctggacg tttcccggct gcggggcggg 120
288 gggagtctcc ggcgcacgcg gccccttggc ccgccccagt cattcccggc cactcgcgac 180
289 ccgaggctgc cgcagggggc gggctgagcg cgtgcgaggc cattggtttg gggccagagt 240
290 gggcgaggcg cggaggtctg gcctataaag tagtcgcgga gacggggtgc tggtttgcgt 300
291 cgtagtctcc tgcaggtctg gggtttccgt tgcagtcctc ggaaccagga cctcggcgtg 360
292 gcctagcgag ttatggcgac gaaggccgtg tgcgtgctga agggcgacgg cccagtgcag 420
293 ggcatcatca atttcgagca gaaggcaagg gctgggaccg ggaggcttgt gttgcgaggc 480
294 cgctcccgac ccgctcgtcc ccccgcgacc ctttgcatgg acgggtcgcc cgccagggct 540
295 agagcagtta agcagcttgc tggaggttca ctggctagaa agtggtcagc ctgggattgc 600
296 atggacggat ttttccactc ccaagtctgg ctgctttta cttcactgtg aggggtaaag 660
297 gtaaatcagc tgtttctttt gttcagaaac tctctccaac tttgcacttt tcttaaagga 720
298 aagtaatgga ccagtgaagg tgtggggaag cattaaagga ctgactgaag gcctgcatgg 780
299 attccatgtt catgagtttg gagataatac agcaggtggg tcataattta gctttttttt 840
300 cttcttctta taaataggct gtaccagtgc aggtcctcac tttaatcctc tatccagaaa 900
301 acacggtggg ccaaaggatg aagagaggta acaagatgct taactcttgt aatcaatggc 960
302 gatacgtttc tggagttcat atggtatact acttgtaaat atgtgcctaa gataattccg 1020
303 tgtttccccc accttttgctt ttgaacttgc tgactcatgt gaaaccctgc tcccaaatgc 1080
304 tggaatgctt ttacttcctg ggcttaaagg aattgacaaa tgggcactta aaacgatttg 1140
305 gttttgtagc atttgattga atatagaact aatacaagtg ccaaagggga actaatacag 1200
306 gaaatgttca tgaacagtac tgtcaaccac tagcaaaatc aatcatcatt tgatgctttt 1260
307 catataggca tgttggagac ttgggcaatg tgactgctga caaagatggt gtggccgatg 1320
308 tgtctattga agattctgtg atctcactct caggagacca ttgcatcatt ggccgcacac 1380
```

Input Set : **A:\new SEQLIST txt.txt**
Output Set: **N:\CRF4\07142006\J700816A.raw**

```
309 tggtggtaag ttttcataaa ggatatgcat aaaacttctt ctaacagtac agtcatgtat 1440
310 ctttcacttt gattgttagt cgcgaattct aagatccaga taaactgtgt ttctgctttt 1500
311 aaactactaa atattagtat atctctctac taggattaat gttattttc taatattatg 1560
312 aggttcttaa acatcttttg ggtattgttg ggaggaggta gtgattactt gacagcccaa 1620
313 agttatcttc ttaaaatttt ttacaggtcc atgaaaaagc agatgacttg ggcaaaggtg 1680
314 gaaatgaaga aagtacaaag acaggaaacg ctggaagtcg tttggcttgt ggtgtaattg 1740
315 ggatcgccca ataaacattc ccttggatgt agtctgaggc cccttaactc atctgttatc 1800
316 ctgctagctg tagaaatgta tcctgataaa cattaaacac tgtaatctta aaagtgtaat 1860
317 tgtgtgactt tttcagagtt gctttaaagt acctgtagtg agaaactgat ttatgatcac 1920
318 ttggaagatt tgtatagttt tataaaactc agttaaaatg tctgtttcaa tgacctgtat 1980
319 tttgccagac ttaaatcaca gatgggtatt aaacttgtca gaatttcttt gtcattcaag 2040
320 cctgtgaata aaaaccctgt atggcactta ttatgaggct attaaaagaa tccaaattca 2100
321 aactaaatta gctctgatac ttatttatat aaacagcttc agtggaacag atttagtaat 2160
322 actaacagtg atagcatttt attttgaaag tgttttgaga ccatcaaaat gcatacttta 2220
323 aaacagcagg tcttttagct aaaactaaca caactctgct tagacaaata ggctgtcctt 2280
324 tgaagctt                                                        2288
```

E--> 325 ~~umy-038~~
E--> 330 ~~1~~   *delete*

```
<210> 1
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> synthetic

<221> misc_feature
<222> 20, 21
<223> n=deoxy thymidine

<400> 1
uggagacuug cgcaaugugn n                                21
```

t's not allowed in an RNA sequence, even if they're represented by n's

for a combined DNA/RNA sequence, use <212> DNA and explain in <220>-<223> section

same error in Seqs. 2-6, 9-14

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/700,816A**

DATE: 07/14/2006

TIME: 09:11:03

Input Set : **A:\new SEQLIST txt.txt**

Output Set: **N:\CRF4\07142006\J700816A.raw**

```
L:32 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:36 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:47 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:62 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:67 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:78 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:93 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:97 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:108 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:112 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:139 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:143 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:154 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:158 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:169 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:184 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:199 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:214 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:218 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:234 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:234 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:234 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:234
L:325 M:254 E: No. of Bases conflict, LENGTH:Input:-38 Counted:2292 SEQ:19
L:325 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=19
L:330 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2288 Found:2292 SEQ:19
```

```
<210> 16
<211> 52
<212> RNA
<213> Artificial Sequence
```
see item 11 on Error Summary Sheet

```
<400> 16
gacaaagaug cuguggccga uaagcuuauc ggccacagca ucuuugucuu uu        52
```